

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/547,660

Source: P45/10

Date Processed by STIC: 9/13/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,660

TIME: 10:16:41

Input Set : A:\Sequence listing - 12810-00125-US.txt

Output Set: N:\CRF4\09132005\J547660.raw

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3 <110> APPLICANT: Hofvander, Per
4      Andersson, Mariette
6 <120> TITLE OF INVENTION: ENHANCED AMYLOSE PRODUCTION IN PLANTS
8 <130> FILE REFERENCE: 12810-00125-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/547,660
C--> 10 <141> CURRENT FILING DATE: 2005-09-01
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002096
11 <151> PRIOR FILING DATE: 2004-03-03
13 <150> PRIOR APPLICATION NUMBER: EP03005181.7
14 <151> PRIOR FILING DATE: 2003-03-07
16 <160> NUMBER OF SEQ ID NOS: 38
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2084
22 <212> TYPE: DNA
23 <213> ORGANISM: Solanum tuberosum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (302)..(1696)
29 <400> SEQUENCE: 1
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34 cacagggggt gcggccattt tttcaccgga atcttcttct ttattttccg gtgaaagttt 180
36 gaacgcacac cgttatttct agacagtga caatgtcaag tgaaaaacat cacaagtttt 240
38 tgaagatttg taattaatta gttgagattt ttaatttgga tgaaagagaa aaacagagaa 300
40 g atg ata ggg cgg gtg ggc ttg ttg ttg gta ttg ttg ata gca acg acg 349
41 Met Ile Gly Arg Val Gly Leu Leu Leu Val Leu Leu Ile Ala Thr Thr
42      1          5          10          15
44 gtg act att ggg gct gaa acg acg acg tta aaa ggg gta aac aga aat 397
45 Val Thr Ile Gly Ala Glu Thr Thr Thr Leu Lys Gly Val Asn Arg Asn
46      20          25          30
48 gcg tat gcg act atg atg tat atg gga act ccg aga gac tac gag ttc 445
49 Ala Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe
50      35          40          45
52 tac gtg gcg act cga gta atg ctc cga tca ctt acc cgg cta gga gtt 493
53 Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
54      50          55          60
56 gaa gcc gat ctc gtc gtt att gct tca ctt gac gtt cct ctt cgc tgg 541
57 Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp
58      65          70          75          80
60 gtt caa act cta gaa gag gaa gat ggt gct aag gtg gtg aga gtt aaa 589
61 Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
62      85          90          95

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64 aat ctg aac aat ccg tat tgt atc aac cct aat tgg aga ttc aag ctc 637
65 Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
66      100      105      110
68 aca ctg aac aaa ctt tat gcg tgg agc ctc gta aat tat gac agg gtt 685
69 Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val
70      115      120      125
72 gtc atg ctt gat gct gac aac ctt ttc ctc cag aaa act gat gaa ctg 733
73 Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
74      130      135      140
76 ttc caa tgt ggc cag ttt tgt gct gtc ttc att aat ccc tgc atc ttc 781
77 Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
78 145      150      155      160
80 cac act ggt ctc ttt gta ttg cag cca tca aaa aag gtg ttc aat gac 829
81 His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
82      165      170      175
84 atg atc cat gag ata gag att ggg agg gaa aat caa gac ggt gca gac 877
85 Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
86      180      185      190
88 caa ggt ttt att gga ggc cac ttc cca gat tta ctt gat cgg cca atg 925
89 Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
90      195      200      205
92 ttc cac cct cct ctt aat ggt acc cag ctc cag gga agt tac agg ctt 973
93 Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
94      210      215      220
96 cct cta gga tac caa atg gac gcc tct tat tat tat ctc aaa ctc cat 1021
97 Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
98 225      230      235      240
100 tgg tcg gta cct tgt gga cct aat agt gtc att aca ttt cct ggt gct 1069
101 Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
102      245      250      255
104 cca tgg tta aaa cca tgg tat tgg tgg tca tgg cct gtc tta ccc ttg 1117
105 Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
106      260      265      270
108 ggc atc cag tgg cat gaa cag cga cgt cta act gtt ggg tat ggt gct 1165
109 Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
110      275      280      285
112 gag atg ata gca gtg ttg atc caa tct ata ttt tac cta gga ata att 1213
113 Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
114      290      295      300
116 gca gtg aca cgc cta gca cgc cca aat tta tca aag ttg tgc tat cgc 1261
117 Ala Val Thr Arg Leu Ala Arg Pro Asn Leu Ser Lys Leu Cys Tyr Arg
118 305      310      315      320
120 cat gat gat agc aag agt gcc ttc tta cta cga act ggc ctt aaa ttg 1309
121 His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
122      325      330      335
124 att gct ata tgg tcc att ctt gct gcc tac aca gtt cct tat ttc gtg 1357
125 Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
126      340      345      350
128 att cct tgt aca gtt cat cca cta gtt ggc tgg agt ctc tac tta ctc 1405

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129 Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
130          355          360          365
132 ggc tct ttt tca cta tcc tgt ata aca gtg aat gca ttt ctt ttg ccg 1453
133 Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
134      370          375          380
136 atg cta cct gtt tta gtc cca tgg att ggg atc ctt ggg gcc ctt ttg 1501
137 Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
138 385          390          395          400
140 gtg atg gct tac cct tgg tac aac gac ggt gtt gta aga gca atg gct 1549
141 Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
142          405          410          415
144 gta ttt aca tac gcc ttc tgt gct tct cca gca tta tgg atg gca ttg 1597
145 Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
146          420          425          430
148 gtt aaa atc aag tgt tct ctt cat gtt tca ctt gag agg gaa gga ttc 1645
149 Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
150      435          440          445
152 ttg ccc aag ata agt gaa tct aca gca cct gct ggt tct aac aaa ctg 1693
153 Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
154      450          455          460
156 tat tgaaagttga aaagttaaag gaatcaacag gagaactaat gcttcagaaa 1746
157 Tyr
158 465
160 catctccaaa cgttttgctt aggagacttg gagtctgctt gtgctatcct agctagttgc 1806
162 ttcagtctgt gctcttaatt agaatggaat tctgtgagtg ggtttagaat tgggaggatg 1866
164 ttttgtgttg tacatggact atctctggtc tcttgaatgc tactccagga aaaagattgt 1926
166 ttctcactta attttttctg ttactaaatt gtatgtggaa taggttcttt aaaatttatt 1986
168 catggattta tgttatgtat gctaacagtg taaatattaa gtcttggtga aataagtaat 2046
170 tccttattca tacaaaaaaa aaaaaaaaaa aaaaaaaaaa 2084
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 465
175 <212> TYPE: PRT
176 <213> ORGANISM: Solanum tuberosum
178 <400> SEQUENCE: 2
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182 Val Thr Ile Gly Ala Glu Thr Thr Thr Leu Lys Gly Val Asn Arg Asn
183          20          25          30
185 Ala Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe
186          35          40          45
188 Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
189          50          55          60
191 Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp
192 65          70          75          80
194 Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
195          85          90          95
197 Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
198          100          105          110
200 Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val

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201          115          120          125
203 Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
204          130          135          140
206 Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
207 145          150          155          160
209 His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
210          165          170          175
212 Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
213          180          185          190
215 Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
216          195          200          205
218 Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
219          210          215          220
221 Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
222 225          230          235          240
224 Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
225          245          250          255
227 Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
228          260          265          270
230 Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
231          275          280          285
233 Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
234          290          295          300
236 Ala Val Thr Arg Leu Ala Arg Pro Asn Leu Ser Lys Leu Cys Tyr Arg
237 305          310          315          320
239 His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
240          325          330          335
242 Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
243          340          345          350
245 Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
246          355          360          365
248 Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
249          370          375          380
251 Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
252 385          390          395          400
254 Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
255          405          410          415
257 Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
258          420          425          430
260 Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
261          435          440          445
263 Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
264          450          455          460
266 Tyr
267 465
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 2230
273 <212> TYPE: DNA
274 <213> ORGANISM: Solanum tuberosum

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Output Set: N:\CRF4\09132005\J547660.raw

276 &lt;220&gt; FEATURE:

277 &lt;221&gt; NAME/KEY: CDS

278 &lt;222&gt; LOCATION: (143)..(2086)

280 &lt;400&gt; SEQUENCE: 3

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281 tatccccaga gaatcagctg aatcaagaac tgatttttag attatgtttt cttgattctt 60
283 tgaaatggga acttgatttt cagtttttca actcagatgt tgtgttcctt tagctggaaa 120
285 acttgaaaaa ggaaagccca ga atg aga gga agt tta gct ggt gga cca cct 172
286                               Met Arg Gly Ser Leu Ala Gly Gly Pro Pro
287                               1           5           10
289 agt cct att gaa cct aga cag agg ctt tct gta ttc act gag gaa aca 220
290 Ser Pro Ile Glu Pro Arg Gln Arg Leu Ser Val Phe Thr Glu Glu Thr
291                               15           20           25
293 agc aaa aga agg ttc ttg aga agt aaa gtt ttc aga gat ggg gag aga 268
294 Ser Lys Arg Arg Phe Leu Arg Ser Lys Val Phe Arg Asp Gly Glu Arg
295                               30           35           40
297 gct ctt cat agt ccc acc aaa aac agg aat ttt acc tgc aag ttc cca 316
298 Ala Leu His Ser Pro Thr Lys Asn Arg Asn Phe Thr Cys Lys Phe Pro
299                               45           50           55
301 act gtg aag ctt ata ttg ggt gtt att gct ctg gtt gca att tgg tca 364
302 Thr Val Lys Leu Ile Leu Gly Val Ile Ala Leu Val Ala Ile Trp Ser
303                               60           65           70
305 ctc tgg cat tct cca gca att tat aac acg gaa tac ata tct agt tca 412
306 Leu Trp His Ser Pro Ala Ile Tyr Asn Thr Glu Tyr Ile Ser Ser Ser
307 75                               80           85           90
309 ggc tct cgg gct gct ttg atg cac aga gag tta agt ggt cat tct tca 460
310 Gly Ser Arg Ala Ala Leu Met His Arg Glu Leu Ser Gly His Ser Ser
311                               95           100          105
313 gct gat caa cgt tat aca tca ctt tta gat att gac tgg gac caa att 508
314 Ala Asp Gln Arg Tyr Thr Ser Leu Leu Asp Ile Asp Trp Asp Gln Ile
315                               110          115          120
317 tcc caa gtt att gag aaa ctg gcc gat agg cat gag tat cag ggc gta 556
318 Ser Gln Val Ile Glu Lys Leu Ala Asp Arg His Glu Tyr Gln Gly Val
319                               125          130          135
321 ggg ata tta aac ttc aat gac agt gaa att gat cag ttg aag gag tta 604
322 Gly Ile Leu Asn Phe Asn Asp Ser Glu Ile Asp Gln Leu Lys Glu Leu
323                               140          145          150
325 cta ccg gac gct gag cat gta atc ttg aac ctg gat cac gtc ccg aat 652
326 Leu Pro Asp Ala Glu His Val Ile Leu Asn Leu Asp His Val Pro Asn
327 155                               160          165          170
329 aat ata aca tgg gaa aca ata tat cct gaa tgg ata gat gaa gaa gaa 700
330 Asn Ile Thr Trp Glu Thr Ile Tyr Pro Glu Trp Ile Asp Glu Glu Glu
331                               175          180          185
333 gaa ttt gag gtc ccc act tgt cct tct ctg ccc aaa att cag ttt ccg 748
334 Glu Phe Glu Val Pro Thr Cys Pro Ser Leu Pro Lys Ile Gln Phe Pro
335                               190          195          200
337 ggt aaa cca agg att gat ctc ata gtt gta aag ctt cca tgc aag aag 796
338 Gly Lys Pro Arg Ile Asp Leu Ile Val Val Lys Leu Pro Cys Lys Lys
339                               205          210          215
341 tct aag gac tgg tat aga gat gta gct cgt ttt cac ttg cag ctg gca 844

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VERIFICATION SUMMARY

DATE: 09/13/2005

PATENT APPLICATION: US/10/547,660

TIME: 10:16:42

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Output Set: N:\CRF4\09132005\J547660.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date